

Db	131	DSQLQITGNGFLSGLKLVDKLYHSEAFTYVNFGEDEAKQINDYVEKGTO	190	Qy	456	AAGAMFLEAIPMSIIPPEVKFNKPFPVFVLMIEONTKSPLFMGKVYNPTOK	503
Qy	276	GKIVDLYKELDRDTVALVNYYFFKGKWERPFEYKDTTEREDFHQVTTVKVPMKRLGM	335	Db	371	AAGAMFLEAIPMSIIPPEVKFNKPFPVFVLMIEONTKSPLFMGKVYNPTOK	418
Db	191	GKIVDLYKELDRDTVALVNYYFFKGKWERPFEYKDTTEREDFHQVTTVKVPMKRLGM	250				
Qy	336	FNIQHCKRLSSWVLLMKYLGNTAATFLPDKGKQHLNELTHDLITKFLENEDRSSL	395		RESULT 3		
Qy	251	FNIQHCKRLSSWVLLMKYLGNTAATFLPDKGKQHLNELTHDLITKFLENEDRSSL	310		ID 000394 PRELIMINARY ;	PRT ;	396 AA.
Db	251	FNIQHCKRLSSWVLLMKYLGNTAATFLPDKGKQHLNELTHDLITKFLENEDRSSL	310		AC 000394 ;		
Db	01-DIC-2001	(TREMBLrel. 19, Created)			AC 000394 ;		
DT	01-DIC-2001	(TREMBLrel. 19, Last sequence update)			DT 01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DE	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 1.				DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
OS	Homo sapiens (Human).				DE Alpha-1-antitrypsin (Fragment),		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Cercopithecus; Cercopithecus.				OS Cercopithecus aethiops (Green monkey) (Grivet).		
OX	NCBI_TaxID=9534;				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.		
RN					OX NCBI_TaxID=9534;		
					RN		
					RP SEQUENCE FROM N.A.		
RC					RC TISSUE="KIDNEY";		
AC					RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinoohara H.;		
CC					RT Cloning and sequencing of complementary DNAs encoding alpha-2-HS glycoprotein, alpha-1-antitrypsin, and beta-actin from african green monkey, Cercopithecus aethiops.;		
DR					RT Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.		
DR					RL [1]		
DR					RN		
DR					RP SEQUENCE FROM N.A.		
DR					RC TISSUE="KIDNEY";		
DR					RX MEDLINE=85026667; PubMed=6333329;		
DR					RN		
DR					RP SEQUENCE FROM N.A.		
DR					RC Colau B., Chichana P., Bollen A.;		
DR					RT Revised sequence of full-length complementary DNA coding for human alpha-1-antitrypsin.;		
DR					RT alpha-1-antitrypsin.;		
DR					RL DNA 3:327-330(1984).		
DR					CC -1 SIMILARITY: BELONGS TO THE SERPIN FAMILY.		
DR					DR AB004044; BAA2024.1. -.		
DR					DR HSSP: P01009; 9 API.		
DR					DR InterPro: IPR00215; Serpin.		
DR					DR Pfam: PF00079; serpin; 1.		
DR					DR SMART: SM00093; SERPIN; 1.		
DR					DR PROSITE: PS00284; SERPIN; 1.		
DR					KW Serpin.		
DR					FT NON-TER 1		
DR					SQ SEQUENCE 396 AA; 1 44587 MW; 1042EABFAA0A2825 CRC64;		
DR					DR 1		
DR					DR 2		
DR					DR 3		
DR					DR 4		
DR					DR 5		
DR					DR 6		
DR					DR 7		
DR					DR 8		
DR					DR 9		
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DR					DR 189		
DR							

Db	302	KTVLGHGITKVFNSGADLGVTEADPLKLSKAVHKAVALTIDEKGTEAAGMFLAEIPMS	361	
Qy	469	IPPEVKENPKFVFLMIENTKSPLMGKVNVNPTQK	503	01-JUN-1998 (TREMBLrel. 06, Created)
Db	362	IPPEVKENPKFVFLMIECQNTKSPLMGKVNVNPTQK	396	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
				01-DEC-2001 (TREMBLrel. 19, Last annotation update)
				Alpha -antitrypsin-like protein.
				OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
				OC Spermophilus
				OX NCBI_TAXID=3179;
				RN [1]
				RP SEQUENCE FROM N.A.
				RC TISSUE-LIVER;
				RX MEDLINE=98094263; PubMed=9434174;
				RA Tokamatsu N., Koijima M., Tanizawa M., Ohba K., Uematsu T., Segawa C.,
				RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
				RT Expression of multiple alpha1-antitrypsin-like genes in hibernating species of the squirrel family.;
				RT Gene 204:127-132(1997).
				RL PROSITE; PS00284; SERPIN; UNKNOWN_1.
				CC [-] SIMILARITY: BELONGS TO THE SERPIN FAMILY.
				DR EMBL; AB00550; BAA24420; 1. -.
				DR BSSP; P01009; 1QLP.
				DR InterPro; IPR000215; Serpin.
				DR Pfam; PF00079; serpin; 1.
				DR SMART; SM00093; SERPIN; 1.
				DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
				KW Serpin.
				SQ SEQUENCE 413 AA; 45953 MW; B08D254695BE0F4 CRC64;
				Query Match 55.3%; Score 1480.5; DB 11; Length 413;
				Best Local Similarity 69.6%; Pred. No. 1.5e-92;
				Matches 282; Conservative 56; Mismatches 62; Indels 5; Gaps 1;
				Qy 97 MGIGSCVSPVKAMDPQGDAQKTFDKFQHPTFKITPMLAEFSYROLAQHSNS 156
				Db 12 LAGLSCLVNGSLAED----AQETGASHHDQEPASRPIAPLAELNQPD 216
				Qy 157 TNIEFSPVSIATAFAMSLGTQKADTHDEILEGLNFNLTEIPAOIHEGFQELLRLNQPD
				Db 67 TNIEFSPVSIAMALASLGTRADTHQIMEGLGFNITETESDHQFGHLLQLTNKP 126
				Qy 217 SQLQTGTNGLFLSEGKFLDVEYKKLYHSEAFVNFGDTEAKQKNDYVKGTOG 276
				Db 127 SQLQTGTNGLFLDHNKLLDKFLQDKLNLYHSEAFSTDNTNEAKQKNTYVKGTOG 186
				Qy 277 KTYDLVKELDRDTYFALVNYIEFKGMWERPEVKTEEDFHVDQVTYKPMKRLGMF 336
				Db 187 KIVDLVLDLNRDSVLAVNYIFFKGKWEKPEVDHTKEEDFHVDQVTYKPMKMRGMNF 246
				Qy 337 NIQHCKLKLSSWVLLMKVGNATAIFPLDEKQLQNLNEHTDITKFLLENDERSAHLH 396
				Db 247 EHYCSTASWVLLQMDLYLGNATAIFPLDEKQLQNLNEHTDITKFLLENDERSAHLH 306
				Qy 397 LPKLSITGTGDKLVSQGLGKTKVNSGADISGYTBEAPLKLSKAVHKAVALTIDEKGTEA 456
				Db 307 FPKLNSTGTMDELKPVLTQLGTTNVSYSKADLSGITEDPLRSVSLHKAVALTIDEKGTEA 366
				Qy 457 AGAMEFLAIPHSIPPEVKFKNPKFLMIEONTKSPLEMGKVVPNT 501
				Db 367 AGATELMMPSLSPPEVKFDKFPLVTVIESTKSPLFVGKVNET 411
				RESULT 6
				P97277 PRELIMINARY; PRT: 413 AA.
				AC P97277; PRELIMINARY; PRT: 413 AA.
				DT 01-MAY-1997 (TREMBLrel. 03, Created)
				DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
				DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
				DE Alpha-1-antiproteinase precursor.
				OS Mesocricetus auratus (Golden hamster).
				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
				OC Mesocricetus.

RESULT 5
054761 ID 054761; PRELIMINARY; PRT; 413 AA.
AC 054761;

Mon Dec 9 12:51:05 2002

DN	NCBI_TAXID=10036;
[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
TISSUE-LIVER;	
XX	MEDLINE=96004895; PubMed=1548212;
XX	Nakatani T., Suzuki Y., Yoshida K., Sinohara H.; "Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-antiproteinase from Syrian hamster: implications for the evolution of Rodentia." ; Biochim. Biophys. Acta 1263:245-248(1995).
RT	-1. SIMILARITY TO THE SERPIN FAMILY.
CC	EMBL; D49709; BA008557.1; -.
DR	HSSP; P01009; QAPI.
RT	InterPro; IPR000215; serpin.
DR	Pfam; PF00073; serpin_1.
RT	SMART; SM00093; SERPIN_1.
KW	Serpin; Signal; PENTENTIAL.
FT	SIGNAL 1 24 ALPHA-1-ANTIPROTEINASE
FT	25 413 AA: 45819 MW: 71D192E106A1EB36 CRC64;
SEQUENCE	413 AA: 56 Mismatches 63; Indels 9; G: Matches 280; Conservative 56; Mismatches 63; Indels 9; G: Matches 280; Best Local Similarity 54.5%; Score 1458.5%; DB 11; Length 413;
SQ	96 GMCGKSCSVPSVKAMEDPQGDAAQKTDTSHHDDQDHPTFNKITTPNLAEFASFLYROLAHQSN : : : : : : : : : : : : : : : : 97 156 STNTIFSPVSTATAPAMLSIQTAKDTHDELLGENENUTIEPPAAQIHGGFOELTRINTQ : : : : : : : : : : : : : : : : Db 66 TNIFIFSPVSTATAPAMLSIQTGKVHTQLEGGFENITIAEEVHGVFHNLQLTQFNRP : : : : : : : : : : : : : : : : : : : : : : : : : : : : : Db 14 DSQLOLTTGNGFLSEGKLIVKDPELVKKLYHSEAFTYNGDTEEAKKQINDYVEKGSTQ : : : : : : : : : : : : : : Db 126 DNELQITTGNGFLIHNKLKVDFKLEEVKNDYHSEAFSYNTFTDSEAAKKVINGVEKGHQ : : : : : : : : : : : : : Db 186 GKIVDLVKDLDRTVALVNYIFFGKWKDGFQKWKPFADNTEADFHVDTKTTVVKPMNSRLGN : : : : : : : : : : : : Db 276 FNIQHCKKLSSVLLMKYLGNAATAIIFLPGKQLEQHETDITLKFELENEDRSASL : : : : : : : : : : : Db 186 EDYHVYSTLSSVLLMDLGNAATAIIFLPGKQMHLEQTKNEELIGKFLKDRTRSANV : : : : : : : : : Db 336 HUPKLSLTGTQDYLKSVLQGLGITKVSNGADLSGYTEAAPLKLSKAVKAVLIDEKGTP : : : : : : : : : : Db 306 HFFKLISGSGTYNEKTLADPLGLTQFENGADISGITEVDPLRGKAVKAVITIDERTGTT : : : : : : : : Db 456 AAGATMFELAIPMSIPIPEVKFKNPFPVFLMIEQNT-KSPLFMGKVYNTQ 502 : : : : : : : : Db 366 AAGATMFELAIPMSVPPENENSPEIALLYDROTASPKSPLFGRVDPTR 413 : : : : : : RESULT 7 064118 PRELIMINARY; PRTR; 406 AA. ID 064118 AC 064118 DT 01-Nov-1996 (TREMBLrel. 01, Created) DT 01-Nov-1996 (TREMBLrel. 01, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Alpha-1-antiproteinase. OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil). OC Meriones; Meizazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae; Meroines. OC NCBITaxonID=10047; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=95155268; PubMed=7852275; RX Goto K., Suzuki Y., Yamamoto K., Sinohara H.; "Plasma alpha-1-antiproteinase from the Mongolian gerbil. Isolation, partial characterization, sequencing of the RT unguiculatus: isolation, partial characterization, sequencing of the RT

RT and implications for molecular evolution."												
RT	J. Biochem. 116: 582-588 (1994).											
RL	-; SIMILARITY: BELONGS TO THE SERPIN FAMILY											
CC	EMBL: S77822; AAB3367.1; -.											
DR	HSSP: P01009; 1OLP.											
DR	InterPro: IPR00215; Serpin.											
DR	Pfam: PF0079; serpin; 1.											
DR	SMART: SM00093; SERPIN; 1.											
KW	Serpin.											
SQ	SEQUENCE 406 AA: 45126 MW: 814613E44C7AA											
Query Match 51.8%; Score 1386; DI												
Best Local Similarity 66.6%; Pred. No. 3.7e-58; Mismatches 58; Matches 271; Conservative												
Qy	96	GMCGKSCVSPVKAMEDPOGDAAQKTDTSHHQDQHPTENI										
Db	14	GIC--CLPSFLSAED--AEKDHS--QDH---										
Qy	156	STNIFPSVSTATAFAMLSELGTKAUTHDEILEGLNFNL										
Db	60	TTNIFLSPSLSTATALAMLGSKDDTKAQLLQLHPEHNL										
Qy	216	DSQLQTTNGNGLFSLGKLVDKFKLFDVKKLYHSEART										
Db	120	DNEQLQTGSSLVFNNSNLNVYKEKLEEVKNHYSEAF										
Qy	276	GKIVDLYKELDRDTVFLAVNLYIFFKGKWRPFKEVPPFKE										
Db	180	GKIVDLYKDLDEIDTVLALAVNLYIFFGKWKPKFPDELLP										
Qy	336	FNIQHQCKKLSSNWVLMKYLGNTAAFFLPDEGKLQHLLIE										
Db	240	EDVHYCDLSSWVLLMDLTGNTAAFFLPDEGKMQHLLIE										
Qy	396	HPLKLSITGTYDIKSVLGQLGITKVSGADLSVTEY										
Db	300	HPLKLSITGTYDIKSVLGQLGITKVSGADLSVTEY										
Qy	456	AAGAMFLIPMSLPPTEYKENPKPEVFLMEOQNTKSPL										
Db	360	AAGTIVLVEAPVMSLPPDVCFKNPPEVVIICDHTQSPL										
RESULT 8												
Q8VC20		PRELIMINARY;		PRT;	413 A							
ID	Q8VC20											
AC	Q8VC20;											
DT	01-MAR-2002	(T-EMBL)el.	20,	Created								
DT	01-MAR-2002	(TRIMB)el.	20,	Last sequence								
DT	01-JUN-2002	(T-EMBL)el.	21,	Last annotation								
DT				Similar to serine protease inhibitor 1-2 (DE protein).								
OS	Mus musculus (Mouse)											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bilateria; Eumetazoa; Deuterostomia; Olfactory epithelium											
OC	Mammalia; Buteraria; Rodentia; Sciurognathi											
OX												
NCBI_TAXID	10090;											
RN	[1]											
RP	SEQUENCE FROM N.A.											
RC	ISSUE-LIVER;											
RA	Strausberg R.											
RL	Submitted (IAN-2002) to the EMBL/GenBank/T											
RP	SEQUENCE FROM N.A.											
RC	ISSUE-LIVER;											
RA	Strausberg R.;											
RL	Submitted (MAR-2002) to the EMBL/GenBank/T											
DR	EMBL: BC022109; AAH22109.1; -.											
DR	EMBL: BC025445; AAH25445.1; -.											
DR	InterPro: IPR00215; Serpin.											
DR	Pfam: PF0079; serpin; 1.											
DR	SMART: SM00093; SERPIN; 1.											
DR	PROSITE: PS00084; SERPIN; UNKNOWN_1.											

KW	Hypothetical protein; Protease.
SEQUENCE	413 AA; 4596 MW; 12C19B63AAD5E66E CRC64;
Query Match	50.5%; Score 1352; DB 11; Length 413;
Best Local Similarity	62.6%; Pred. No. 7, 8e-84;
Matches	256; Conservative 73; Mismatches 70; Indels 10; Gaps 4;
Qy	96 GMCKSCVSPVKAMEDPOGDAAKQTDTSHDDHPTENKTPNLAEEFAFSYROLAQHN 155
Db	14 GLC---CLVPSFLAED----VQETDSQDQS-PASHEATNLDFASFLSYRELHQHN 64
Qy	156 STNIFSPVSIATAFAMISLGTKADTHDEILEGLNFNLTEPEAQIHEGFQELLRLNQP 215
Db	65 TSNIFSPVSIATAFAMISLGSKGDHTQLEGLOENLTOTSEADIHKSFQHLJLQTLPNRP 124
Qy	216 DSQOLTTGNGLFLSSEGKLLVDKFLEDKKKLYGNATAIFPLDGGKQHLENELTHDITKFLENEDRRSASL 275
Db	125 DSEQLSTGNGLEVNDLKLVEKFLEAKNHQAEVFSNFAESEAKVINDFVEKGQT 181
Qy	276 GKIVDLYKELDRTVFALVNIEFKCKWERPEVKDTEEDFHQVTTVKVPMKRLGM 335
Db	185 GKIVAEYKQLDDDTVALANYLFGKWKWPDPNTAEFHVDESTVVKVMMTLSGM 241
Qy	336 FNIQHCKKLSSVLLAKYLNQATAIFPLDGGKQHLENELTHDITKFLENEDRRSASL 395
Db	242 LDVHHCSTLSSVLLAKYDAGNATAVFLPDGKQHOLEQTLSKELISFELLNRRLAQI 301
Qy	396 HPLKLSGTGTVDLKSVLQGLGKITYFNSGADLSVTE-APLKLSKAYHKAVLTIDENG 454
Db	302 HPRLSTGSEVNLKTLMSPUGITRFFNGADLSGTEENAPLKSQAHKAVLTIDETGT 361
Qy	455 EAAGAMFLAIPMSIPPEVKFNPKEFLMEOQNTSPLEMGKVYNPDK 503
Db	362 EAAAVTVLLAVPSMPILRFDPHPLFIFEEHQSPLEVGKVVDPTIK 410
RESULT 10	
Q91XB8	PRELIMINARY; PRT; 413 AA.
ID	Q91XB8; ID Q91XB8;
AC	Q91XB8; AC Q91XB8;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Similar to serine protease inhibitor 1-1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-LIVER;
RA	Strausberg R.; RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL	CC - SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR	EMBL; BC011040; AAH11040; 1.
DR	InterPro; IPR000215; Serpin.
DR	Pfam; PF00079; serpin; 1.
DR	PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW	protease; Serpin.
SQ	SEQUENCE: 413 AA; 4566 MW; A1FDA1B0C96FDCC CRC64;
Query Match	50.3%; Score 1346; DB 11; Length 413;
Best Local Similarity	62.3%; Pred. No. 2e-83;
Matches	255; Conservative 72; Mismatches 72; Indels 10; Gaps 4;
RA	Strausberg R.; RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL	CC - SIMILARITY: BELOWS TO THE SERPIN FAMILY.
DR	EMBL; BC015266; AAH15266; 1.
DR	InterPro; IPR000215; Serpin.
DR	Pfam; PF00079; serpin; 1.
DR	PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW	Hypothetical protein; Serpin.
FT	NON_TER 1
SO	SEQUENCE: 410 AA; 45622 MW; ED142591DB58F5E2 CRC64;
Query Match	50.3%; Score 1346; DB 11; Length 410;
Best Local Similarity	62.8%; Pred. No. 2e-83;
Matches	257; Conservative 70; Mismatches 72; Indels 10; Gaps 4;
Qy	96 GMCKSCVSPVKAMEDPOGDAAKQTDTSHDDHPTENKTPNLAEEFAFSYROLAQHN 155
Db	11 GLC---CLVPSFLAED----VQETDSQDQS-PASHEATNLDFASLYRELHQHN 61
Qy	156 STNIFSPVSIATAFAMISLGTKADPHDEILEGLNFNLTEPEAQIHEGFQELLRLNQP 215
Db	62 TSNIFSPVSIATAFAMISLGSKGDHTQLEGLOFNLTQTSEADIHKSFQHLJLQTLPNRP 121
Qy	156 STNIFSPVSIATAFAMISLGTKADPHDEILEGLNFNLTEPEAQIHEGFQELLRLNQP 215
Db	62 TSNIFSPVSIATAFAMISLGSKGDHTQLEGLOFNLTQTSEADIHKSFQHLJLQTLPNRP 121
Qy	216 DSQOLTTGNGLFLSSEGKLLVDKFLEDKKKLYGNATAIFPLDGGKQHLENELTHDITKFLENEDRRSASL 395
Db	245 LDVHHCSTLSSVLLAKYDAGNATAVFLPDGKQHOLEQTLSKELISFELLNRRLAQI 304
Qy	296 HPLKLSGTGTVDLKSVLQGLGKITYFNSGADLSGTEENAPLKSQAHKAVLTIDEGT 454

Db	305 HPPRLISGENNLKTMSPGLITRINNGAELSGTTEENAPLKLSSQVHKAVLTIDETGT	364
Qy	455 EAAGAMFLEAPMSIPEVKENPKPFYLMIEONTKSPLEFMGKVNPYTK 503 : : : : : : : : : : : : : :	503
Db	365 EAAATVLLAVY SMPILRDHPFLFILLEHTQSPLFVSKVDPYHK 413	413

RESULT 11				
91WV74	Q9IVY4; Q9LV74;	PRELIMINARY;	PRT;	413 AA.
D	01-DEC-2001 (TREMBLrel. 19, Created)			
C	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
T	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
T	Unknown (Protein for MGC:13995) (Similar to serine protease inhibitor 1-3) (Protein for MGC:13994) (Hypothetical 46.0 kDa protein).			
E	Mus musculus (Mouse).			
S	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Furbaria; Schizoramphida; Muridae; Murinae; Mus.			
C				

RESULT	ID	PRELIMINARY;	PRT;	413 AA.
12	Q28665			
	Q28665;			
	AC	01-NOV-1996 (TREMBLrel. 01, Created)		
	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
	DS	Alpha-1-antiprotease E precursor.		
	OS	Oryctolagus cuniculus (Rabbit).		
	OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.		
	OC			
	OX	NCBI_TaxID=9986;		

P SEQUENCE FROM N.A.
P Strausberg R.;
I Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
[2]
N
P SEQUENCE FROM N.A.
P TISSUE-LIVER;
C Strausberg R.;
I Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
[3]
N
P SEQUENCE FROM N.A.

RA Saito A., Shinohara H.;
 RT "Rabbit alpha-1-antiprotease E: a novel recombinant serpin which
 does not inhibit proteinases.";
 RIL Biochem. J. 307: 369-375 (1995).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BAA04579.; -.
 DR HSSP; P01009; BAPI.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00001; SERPIN_1.
 DR

ID	Q91XCI	PRELIMINARY;	PRT;	425 AA.	RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
AC	Q91XCI;				DR EMBL; BC021850; AAH21850_1; -.
DT	01-JEC-2001 (TREMBLeL 19, Created)				DR InterPro; IPR000215; Serpin.
DT	01-DEC-2001 (TREMBLeL 19, Last sequence update)				DR Pfam; PF00079; serpin_1.
DT	01-MAR-2002 (TREMBLeL 20, Last annotation update)				DR SMART; SM0093; SERPIN_1.
DE	Unknown (Protein for IMAGE:4210562) (Fragment).				DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
OS	Mus musculus (Mouse).				KW Protease.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				KW
OC	NCBI_TaxID=10090;				SQ SEQUENCE
OX				413 AA;	45995 MW;
RN	[1]				C9644EC0A7951872 CRC64;
RP	SEQUENCE FROM N.A.				Query Match Score 49.9%; Best Local Similarity 49.9%; Pred. No. 1.1e-82; Gaps 4;
RC	TISSUE=LIVER;				SEQUENCE FROM N.A.
RA	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
RL	CC 1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
DR	EMBL; BCO10988; AAH10988_1; -.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
DR	InterPro; IPR000215; Serpin.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
PFam;	PF00079; serpin_1.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
DR	PROSITE; PS00284; SERPIN; UNKNOWN_1.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
KW	Serpin.				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
FT	NON_TER 1				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
SQ	SEQUENCE 425 AA;	1			Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Score 4715 MW;	EA9E50E40C33CAF C RC64;				Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Query Match Score 1342; DB 11; Length 425;					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Best Local Similarity 62.6%; Pred. No. 3.9e-87;					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Matches 256; Conservative 70; Mismatches 73; Indels 10; Gaps 4;					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 96 GMCGKSCSVPSVKAMEDPQQGDAAKQTDTSHHDQDPFKPNKTPNLAEFAFSLYROLAHSN 155					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 26 GLC---CLVPSFLAED---VOETDSQKQGS-PASHEATNLGDFAIISLYRELHQSN 76					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 156 STNIFSPVSTATAFAMLSLGTKADTHDEILEGLNFNLTEPEAQTHEGFOELLTLNQF 215					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 77 TSNIFSPVSTATAFAMLSLGTKADTHDEILEGLNFNLTEPEAQTHEGFOELLTLNQF 215					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 77 TSNIFSPVSTATAFAMLSLGTKADTHDEILEGLNFNLTEPEAQTHEGFOELLTLNQF 215					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 216 DSQLQUTTGNGLFLSSEGKLVYDQNLQTLTQILEGLQNLQTSEADTHKSFQHLQTLNRP 136					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 137 DSELQSLSTGNGLFVNNDLKLVEKFLEAKVHYQAEVFSVNAESEBAKVVINDPEVKGTQ 196					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 276 GKIVDLVKELORDVTALVALVYIFFKGKWERPFEVKDTEEEFDHYDQVTTVKVPNMKRIGM 335					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 197 GKAIAEAVKKLQDQTPEALAVNLFLGKWKPFDPENTEEAFHYDESTTVKVPNMRTSCM 256					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 336 ENIQHQCKKLSSWLLMKYLGNATAKEFLPDEGKLOHLENLTHDLITKFNEEDRSASE 395					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 257 LDVHHESTLSSWLWLDYAGATAFLPDLGKQMHLEQTLSKELISKELLNRRRLQI 316					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 396 HLPKLSITGTDLKSYLVGLQGITKVFSNGADLSGVTE-APLKSKAVHLVLTIDEKT 454					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 317 HFPRLSTSGEYNKLTMSPGLTRIFNNNGADLSGTEENPIKLSQAVHKAVLTIDEKT 376					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
QY 455 EAAGAMFLEATPMSIPEPVRENKPPEVFLMEEQNTKSPLFPGKVNNTPKQ 503					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
Db 377 EAAAVTVLLAVPYSMPPILFITEEHTQSPLFFVGKVVDPTHK 425					Best Local Similarity 62.3%; Pred. No. 1.1e-82; Gaps 4;
RESULT 14					SEQUENCE FROM N.A.
Q8VC41	PRELIMINARY;	PRT;	413 AA.		SEQUENCE FROM N.A.
AC	Q8VC41;				RC TISSUE=LIVER;
DT	01-MAR-2002 (TREMBLeL 20, Created)				RA Salto A.;
DT	01-AUG-1998 (TREMBLeL 07, Last sequence update)				RT "Proteinase inhibitory activity of recombinant alpha-1-antiproteinases expressed in Escherichia coli."
DE	Similar to serine protease inhibitor 1-4.				RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
OC	NCBI_TaxID=10090;				DR ENSP; P01009; BAP1.
OC	SEQUENCE FROM N.A.				DR InterPro; IPR000215; Serpin.
RC	TISSUE=LIVER;				DR Pfam; PF00079; serpin_1.
RA	Strausberg R.;				DR SMART; SM0093; SERPIN_1.
RA					DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW	Serpin.				DR Sequence FROM N.A.
SQ	SEQUENCE 456 AA;	50542 MW;			RT TISSUE=LIVER;
Score 88E19DEF2767F5C07 CRC64;					RA Salto A.;
Best Local Similarity 58.8%; Pred. No. 2e-82;					RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
Length 456;					CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

	Matches	266;	Conservative	65;	Mismatches	105;	Indels	16;	Gaps	4;
Qy	54	T P N P T R K E G K C P V T Y G O O L M A P P N F C E - -	- D I G Q Q C K R D I C R U C M G R C K S V S P Y K A M E	110						
Db	17	T P S P T S S E W A S P - - -	S L I P P A L D T E S W T M P P S Y S R A L - - -	63						
Qy	111	D P O G D A A Q T D S H D O D H P T F N K I T P N I A E F A S L Y R O L A H O S N S T N I F F S P V S T A T A F	170							
Db	64	G F L A D E A Q E A V S S H E Q D I P A C H T I A P S A E F A S I F	P R E V A R E S N T N I F F S P V S I S A F	123						
Qy	171	A M L S I G T K A D T H D E L E G L N F N T E I P A Q I H E S F Q E L L R T I N Q P D S O L Q T T G N G I F L S	230							
Db	124	A M L S L G A K G P H T Q V E G I K F N K P E T E A Q I H D G F R H L H T W P R D S E L Q L A G N A L V H	183							
Qy	231	E G L K L V D K F L E D V K L L H S A F T I N G D T E A K Q I N D Y V E K S T O G K Y D I A K E L D R T Y	290							
Db	184	E N L K L Q H K F L E D A K N Y Q O S E A F L Y D F R D P E Q A K T K I N S H E V E K T R G K T V D I Q E L D A R T L	243							
Qy	291	F A L V N Y T F F G K W E R P F E Y K D T E E B D H V D Q V T V K V P M M K R G M F N I O H C K K L L S S V N L L	350							
Db	244	I A L V N V V F F R G K W E R P F E P P M T K E E D H V D A T T V Y R P M M S R I G M Y T L H C S T A S T V L	303							
Qy	351	M K Y L G N A T A I F E L P D E G K L Q H L E N E L T H D I T T K F L E N E D R R S A S L H P K L I S T I G Y D L K S	410							
Db	304	M D Y K G N A T A L E L L P D E G K L Q H L E D D L T E L A K T K L S S I R S V T V R F P L S I S T Y D L K P	363							
Qy	411	V I G Q L G I T K V E S N G A D L S G V T E E A P K L S K A V H K A V L T I D E K G T E A A G M F L E A I P M S I P	470							
Db	364	I L G K L G I T Q V E S D N T O L S G T E Q E A L K V S A L A H K A V L T I D E R G T E A A G T F V E X V L Y S M P	423							
Qy	471	P E V K E N K P F V F I L M I O N T K S P L E M G K V V N P T Q	502							
Db	424	Q R V T F D R P F I V Y S H E V K S P L F V G R V D P Q	455							

Search completed: November 30, 2002, 12:36:43
Job time : 23.5 secs